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EXAMINER	
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ART UNIT	PAPER NUMBER
1638	

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/523,503	MITTENDORF ET AL.	
	Examiner	Art Unit	
	BRENDAN O. BAGGOT	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on *04 March 2008*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-3,6-16,20-22,24-40 and 42* is/are pending in the application.

4a) Of the above claim(s) *14,15,25-32,35 and 36* is/are withdrawn from consideration.

5)☒ Claim(s) *21 and 22* is/are allowed.

6)☒ Claim(s) *1-3,6-13,16,20,24,33,34,37-40 and 42* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☒ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *See Office Action*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Restriction / Election

1. Claims 15, 25-32 and 35-36 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention, there being no allowable generic or linking claim.

2. Applicant's election with traverse of Group XII, claims 1-3, 6-14, 16, 20-22, 24, 33-34, 37-40 and 42, drawn to SEQ ID NO: 23 encoding SEQ ID NO: 24 in the reply filed on 3/4/08 is acknowledged. The traversal is primarily on the ground(s) that Applicants believe there is no undue search burden. This is not found persuasive because individual sequences are deemed independent inventions rather than species of a genus, Patent Office resources prohibit the searching in a single application of multiple non-identical sequences against the more than 59,000,000,000 bases in Genbank, and there is no search burden requirement for restriction/lack of unity under 371 cases. While a search of the prior art for one group may overlap with that of another group, they are not co-extensive of each other and thus would represent undue burden on Office resources. The requirement is still deemed proper and is therefore made FINAL.

3. The requirement is still deemed proper and is therefore made FINAL.

4. Applicant is reminded that upon the cancellation of claims to a non-elected invention, the inventorship must be amended in compliance with 37 CFR 1.48(b) if one or more of the currently named inventors is no longer an inventor of at least one claim remaining in the application. Any amendment of inventorship must be accompanied by a request under 37 CFR 1.48(b) and by the fee required under 37 CFR 1.17(i).

5. Claims 15, 25-32 and 35-36 are nonelected. Claims 1-3, 6-14, 16, 20-22, 24, 33-34, 37-40 and 42, drawn to SEQ ID NO: 23 are pending and examined in the instant application.

Specification

6. Applicant is required to update the status (pending, allowed, etc.) of all parent priority applications in the first line of the specification. The status of all citations of US filed applications in the specification should also be updated where appropriate.

7. The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser executable code. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. *See* M.P.E.P. § 608.01. *See* page 59 for example.

Information Disclosure Statement

8. An initialed and dated copy of the information disclosure statements (IDS) submitted on 3/9/05, 5/16/05, 9/8/06, 6/18/07 are attached.

Claim Objections

9. Claims 1-3, 11-13, 24, 34, 37 and their dependent claims are objected to as being drawn to nonelected sequence embodiments.

Claim Rejections - 35 U.S.C. §112, second paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

10. Claims 21, 22, and 24 is rejected under 35 U.S.C. §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which the applicant regards as the invention.

11. In Claim 21, the metes and bounds of "wherein the LMP nucleic acid comprises a first nucleic acid that hybridizes" is unclear because "a first nucleic acid" implies that there are two nucleic acids. Does the claim encompass more than the elected SEQ ID NO: 23? Clarification and / or correction are required.

12. In Claim 21 and 22, it is unclear how the complement of SEQ ID NO: 23 will code for a protein. The art does not recognize that the antisense strand of a gene will encode for a protein. Clarification and / or correction are required.

13. Claim 24 is rejected under 35 U.S.C. 112, second paragraph, as being incomplete for omitting essential steps, such omission amounting to a gap between the steps. See MPEP § 2172.01. The omitted step is: modification of expression of digalactosyl diacylglycerol synthase (DGDG), the use of a structural element which results in the modification of expression such a tissues specific promoter, a step of sense or antisense expression. Clarification and / or correction are required.

14. Claim 24 is rejected under 35 U.S.C. 112, second paragraph, as being incomplete for omitting essential steps, such omission amounting to a gap between the steps. See MPEP § 2172.01. The omitted step is: plant transformation resulting in a transgenic plant that expresses the transgene having the activity of the claimed activity. Applicant is encouraged to put the activity in the claims due to the percent identity language. Clarification and / or correction are required.

15. Claim 24 recites the limitation "wherein the LMP nucleic acid comprises a . . . [complement] . . . of the full-length LMP nucleic acid of a) or b) above." Paragraph 52 of the specification describes a LMP as a sequence as shown in Appendix A. Appendix A shows only the sense strand and the protein encoded thereby. It is unclear how a LMP is both the sense and the antisense strand. Applicant implies that the sense and antisense strands are both LMPs. Clarification and / or correction are required.

16. Regarding applicant's recitation of "complement", it is unclear whether "complement" is intended to be fully complementary or whether a partial complementarity such as a single base pair would be encompassed by Applicant's recitation of "complement."

17. Regarding applicant's recitation of "stringency conditions" it is unclear what is encompassed by stringency conditions" since skilled artisans can and do define stringency conditions differently and Applicant has not properly defined "stringency conditions." (See paragraphs 42 and 51 of the Specification).

> [0042] . . . In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a polynucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to one of the polynucleotide sequences shown in Appendix A, or a portion thereof. These *stringent conditions include* washing with a solution having a salt concentration of about 0.02 M at pH 7 and about 60.degree. C. In another embodiment, the stringent conditions comprise an initial hybridization in a 6.times. sodium chloride/sodium citrate (6.times.SSC) solution at 65.degree. C.
>
> [0051] . . . As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75%, or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those skilled in the art and can be found in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6.times. sodium chloride/sodium citrate (SSC) at about 45.degree. C., followed by one or more washes in 0.2.times.SSC, 0.1% SDS at 50-65C. In another embodiment, the stringent conditions comprise an initial hybridization in a 6.times. sodium chloride/sodium citrate (6.times.SSC) solution at 65.degree. C. . . ..

Claim Rejections - 35 U.S.C. §112, first paragraph, enablement

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

18. Claims 1-3, 6-14, 16, 20-22, 24, 33-34, 37-40 and 42 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for SEQ ID NO: 23, plants transformed therewith, and a method of producing a transgenic plant having a modified level of a seed storage compound, does not reasonably provide enablement for complements, "hybridizants" or sequences 70% identical to SEQ ID NO: 23 or a method of producing a transgenic plant having a modified level of a seed storage compound and wherein the polynucleotide sequence is a SEQ ID NO: 23-complement . The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

Applicant's claims are broadly drawn to expression of SEQ ID NO: 23, hybridizants, complements, and sequences 70% identical to SEQ ID NO: 23. Applicants teach sense expression and sequences 100% identical to SEQ ID NO: 23. Applicants do not teach expression of any hybridizant, complement, or sequence 70% identical to SEQ ID NO: 23 that modulates seed storage compounds, "hybridizants" or sequences 70% identical to SEQ ID NO: 23.

Applicant is claiming complementary sequences and sequences that hybridize. These sequences are not enabled for modulating a seed storage compound in a plant. It appears that

such sequences could only be used as antisense sequences to inhibit expression of some compound.

There is abundant prior art to suggest that antisense expression is difficult, unpredictable and unsuccessful. It is well known in the art that out of the large number of nucleic acid sequences complementary to a given transcript, only a portion are effective at inhibiting expression of the gene as shown by Stein et al (Nature Biotechnol. (March 1999) 17:209) who states it has been a frequent, perhaps even universal, observation that for every eight or so oligomers tested against any one particular target, only one will be active. In fact, the ratio of 1 success in 8 tested seems to be the best ratio attained, some researches report 1 success in 12 or, or even 1 in 15 (page 209, column 2). Effective sequences can not be predicted and must be identified experimentally and tested experimentally. The specification provides guidance on sense expression of sequences 100% identical to SEQ ID NO: 23, but this guidance is not sufficient to allow one to make and use antisense expression of sequences 70% identical to SEQ ID NO: 23. In a technical discipline which requires specific sequences for function, the artisan would not be able to make and use the invention as broadly claimed. Bartoszewski, et al., teaches (2002, J. Amer. Hort. Sco. 127(4):535-539) that attempts to transform more than 1400 explants with a sense or antisense construct *produced no transgenic plants*. Bartoszewksi also teaches the complete failure to produce even a single transgenic plant transformed with EITHER a sense construct or an antisense construct which was 75% identical to the targeted gene. (See abstract; p. 538, r. col. last para.).

That Bartoszewski used an antisense construct with 75% identity as opposed to the 70% identity claimed by Applicants is not dispositive. If Bartoszewksi used a fragment with high

homology on the 5' end of the gene but somewhat looser homology further downstream, it is quite possible that Bartoszewski could achieve reductions in transcript levels with a sequence which is only 75% identical overall, but higher identity in the critical 5' region of the gene.

Applicant has no working examples of sense or antisense expression of any sequence that modulates seed storage compounds, "hybridizants" or sequences 70% identical to SEQ ID NO: 23 in plants.

It is well established that sequence similarity, e.g., at least 70% identical, is not sufficient to determine functionality of a coding sequence. See the teachings of Doerks (TIG 14, no. 6: 248-250, June 1998), where it states that computer analysis of genome sequences is flawed, and "overpredictions are common because the highest scoring database protein does not necessarily share the same or even similar function's" (the last sentence of the first paragraph of page 2484). Doerks also teaches homologs that did not have the same catalytic activity because active site residues were not conserved (page 248, the first sentence of the last paragraph).

Neither the state of art nor Applicants provide guidance as to how inoperable embodiments can be readily eliminated other than random trial and error. In the absence of guidance, it would have been highly unpredictable at the time the claimed invention was made that a DNA sequence which is at least 70% identical to SEQ ID NO: 23 would encode a functionally active enzyme that has the ability to modulate seed storage compounds in a plant. Undue experimentation would have been required by a skilled artisan to determine how to use a DNA sequence which has at least 70% sequence identity to SEQ ID NO: 23 in a method that would modulate seed storage compounds in a plant.

The state-of-the-art is such that one of skill in the art cannot predictably undertake identification of functional gene sequences by percent identity to a known sequence or gene identification via hybridization. Truksa, et al teach that they could only *suggest* that the described cDNAs were conlinin cDNAs (emphasis added). (2002) Plant Physiology and Biochemistry, Volume 41, Number 2, 1 February 2003, pp. (7) *See* page 144-145. Truksa's teaching supports a conclusion that putative structural genes isolated by hybridization and which hybridize or which are complementary are not enabled and would require undue experimentation to determine if the hybridizing sequences were in fact structural genes. It is well established that sequence similarity is not sufficient to determine functionality of a coding sequence. See the teachings of Doerks (TIG 14, no. 6: 248-250, June 1998), where it states that computer analysis of genome sequences is flawed, and "overpredictions are common because the highest scoring database protein does not necessarily share the same or even similar function's" (the last sentence of the first paragraph of page 2484). Doerks also teaches homologs that did not have the same catalytic activity because active site residues were not conserved (page 248, the first sentence of the last paragraph).

In the instant case, along with the absence of working examples, the relatively small amount of guidance in the specification, the unpredictability in the art and the large amount of experimentation would be necessary to achieve function balanced only against the high skill level in the art, it is concluded that it would require undue experimentation for one of skill in the art to perform the method of the claim as broadly written.

Claim Rejections - 35 U.S.C. §102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

35 U.S.C. §102.

19. Claims 1-3 and 6-9 are rejected under 35 U.S.C. 102(e) as being anticipated by Levin *et al.* ("Levin -2," WO/2003/008440 (SEQ ID NO: 41)), filed 7/16/02). Levin-2 teaches a nucleic acid comprising SEQ ID NO: 23, that SEQ ID NO: 23 is a DGDG (digalactosyl diacylglycerol synthase (DGDG) and its expression (via an expression vector) in *E. coli.*

A sequence which anticipates a sequence which is 100% identical to SEQ ID NO: 24 also anticipates a sequence at least 70% or at least 90% identical to SEQ ID NO: 24. Thus, the reference teaches all the limitations of the Claimed invention. A sequence which anticipates a sequence which is 100% identical to SEQ ID NO: 23 also anticipates the complement and hybridizant of SEQ ID NO: 23. SEQ ID NO: 23 is a double stranded polynucleotide. Because Levin cloned SEQ ID NO: 23 (Levin's SEQ ID NO: 41) into a well-known double stranded DNA expression vector and then into E. coli., the presence of the complement is inherent because the vector is double stranded and it is isolated. Because the full complement would hybridize to SEQ ID NO: 23 under unspecified stringency conditions, Levin anticipates a sequence which comprises a nucleic acid which would hybridize to SEQ ID NO: 23, namely the complement. Thus, the reference teaches all the limitations of the claimed invention.

20. Claims 1-3, 6-13, 16, 20-22, 24, 33-34 are rejected under 35 U.S.C. 102(b) as being anticipated by Dormann *et al.* (*Arabidopsis* Galactolipid biosynthesis and lipid trafficking mediated by DGD1, Science 284:2181-2184). Dormann complemented the DGD1 (encoding DGDG, Genbank Accession No.s AF149842, AF149841) locus of an Arabidopsis knockout dicot oilseed plant by transgenic expression of DGDG using Genbank Accession No.s AF149842, AF149841AF, identical to Applicant's SEQ ID NO: 23. SEQ ID NO: 23 is the Arabidopsis DGDG (See page 2183; Genbank Accession No.s AF149842, AF149841AF). Dormann therefore discloses a sequence 100% identical to SEQ ID NO: 23, complemented transgenic plants expressing SEQ ID NO: 24 (DGDG enzyme) under the control of the constitutive P35S promoter. The P35S promoter is a well-known non-tissue specific promoter. Because the vector of Dormann complemented the DGDG knockout, it was an expression vector. Dormann's complimented DGDG-knockout is a transgenic plant with an expression vector expressing the DGDG gene behind the P35S promoter wherein the product of the expression vector gets expressed; wherein the gene expressed is SEQ ID NO: 23 and therefore has an LMP domain because it is the same sequence as applicant's sequence; wherein SEQ ID NO: 24 is expressed because it is the product of SEQ ID NO: 23 expression; wherein the LMP polynucleotide has at least 70% identity with SEQ ID NO: 23 (Dormann's sequence is 100% identical); wherein the polypeptide encoded is SEQ ID NO: 24. (*Id.* @ footnotes 18, 20, p. 2183, r. col., first paragraph; *See* entire document).

With respect to claims 33 and 34, because Dormann's sequence is the same as Applicant's, it inherently contains a lipid metabolism domain.

A sequence which anticipates a sequence which is 100% identical to SEQ ID NO: 24 also anticipates a sequence at least 70% or at least 90% identical to SEQ ID NO: 24.

A sequence which anticipates a sequence which is 100% identical to SEQ ID NO: 23 also anticipates the complement and hybridizant of SEQ ID NO: 23. Because Dormann uses SEQ ID NO: 23, Dorman's sequence inherently meets the limitations of claims 1-3. (*Id.* @ footnotes 18, 20, p. 2183, r. col., first paragraph; *See* entire document). SEQ ID NO: 23 is a double stranded polynucleotide. Because Dormann cloned SEQ ID NO: 23 (Dormann SEQ ID NO: 41) into a well-known double stranded DNA expression vector and then into *Arabidopsis thaliana*, the presence of the complement is inherent because the vector is double stranded and it is isolated. Because the full complement would hybridize to SEQ ID NO: 23 under unspecified stringency conditions, Dormann anticipates a sequence which comprises a nucleic acid which would hybridize to SEQ ID NO: 23: namely the complement.

Thus, the reference discloses all the limitations of the Claimed invention.

Claim Rejections - 35 U.S.C. §103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

35 U.S.C. §103(a).

The *Graham* court set forth the factual inquiries that are applied for determining obviousness under 35 U.S.C. 103(a):

1. Determining the scope and contents of the prior art.
2. Ascertaining the differences between the prior art and the claims at issue.
3. Resolving the level of ordinary skill in the pertinent art.
4. Considering objective evidence present in the application indicating obviousness or nonobviousness.

Graham v. John Deere Co., 383 U.S. 1, 148 USPQ 459 (1966).

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

21. Claims 1-3, 6-14, 16, 20-22, 24, 33-34, 37-40 and 42 are rejected under 35 U.S.C. 103(a) as being unpatentable over Levin *et al.* ("Levin -2," WO/2003/008440 (SEQ ID NO: 41), filed 7/16/02) or Dormann *et al.* (*Arabidopsis* Galactolipid biosynthesis and lipid trafficking mediated by DGD1, Science 284:2181-2184) in view of Goodman (4956282 (B) US, 1990).

Levin-2's teachings are discussed above.

Dormann's teachings are discussed above.

Dormann also teaches an isolated Lipid Metabolism Protein (LMP) nucleic acid comprising a polynucleotide sequence encoding a polypeptide that functions as a modulator of a seed storage compound in a plant, wherein the polynucleotide sequence is 100% identical to SEQ ID NO: 23 encoding SEQ ID NO:24; an expression vector; and a non-tissue-specific promoter. (*Id.* @ footnotes 18, 20, p. 2183, r. col., first paragraph; *See* entire document).

Dormann also teaches a method of producing a transgenic plant having a modified level of a seed storage compound comprising, transforming a plant cell with an expression vector comprising a lipid metabolism protein (LMP) nucleic acid and generating from the plant cell the transgenic plant, wherein the nucleic acid encodes a polypeptide that functions as a modulator of a seed storage compound in the plant, and wherein the nucleic acid comprises SEQ ID NO:23 encoding SEQ ID NO:24. (*Id.* @ footnotes 18, 20, p. 2183, r. col., first paragraph; *See* entire document).

Dormann also teaches a method of modulating the level of a seed storage compound in a plant comprising modifying the expression of a LMP nucleic acid in the plant, wherein the LMP nucleic acid comprises SEQ ID NO:23 encoding SEQ ID NO:24 and contains a lipid metabolism domain. Dormann teaches a transgenic plant made by a method comprising transforming a plant cell with an expression vector comprising SEQ ID NO:23, and generating from the plant cell the transgenic plant, wherein expression of the SEQ ID NO:23 in the plant results in a normal level of a seed storage compound in the plant; a dicotyledonous or monocotyledonous oil producing plant species. (*Id.* @ footnotes 18, 20, p. 2183, r. col., first paragraph; *See* entire document) as compared to wildtype.

Neither Levin nor Dormann teach monocot or modified or increased as compared to the wild type variety of the plant.

Goodman teaches the expression of heterologous proteins in monocot and dicot plants. Because the plants of Goodman do not require complementation of the DGDG locus, expression of the SEQ ID NO: 23 of Dormann would result in modified and increased level of the seed

storage compound in the transgenic plant as compared to the wild type variety of the plant (Col. 4, Ln.s 58-61).

It would have been *prima facie* obvious to one skilled in the art at the time the invention was made to substitute the heterologous protein of Goodman with the LMP proteins of Levin-2 (FAD2) or Dormann (DGDG) and express DGDG in plants for the purpose of "investigating galactolipid biosynthesis and subcellular lipid trafficking" as taught by Dormann in any desired plant such as corn, soybean, etc. as taught by Goodman. One would have been motivated to do so to obtain a greater understanding of galactolipid biosynthesis and subcellular lipid trafficking. One would have done so with a reasonable expectation of success because Dormann successfully expressed DGDG in *Arabidopsis* plants.

Comment

The prior art made of record and not relied upon is considered pertinent to applicant's disclosure. Levin *et al.* (Levin -1, N_Geneseq Database. Accession No. ADB95043, WO/2003/008440 (SEQ ID NO: 41), published 30 January 2003) teaches SEQ ID NO: 23 encoding SEQ ID NO: 24.

22. All Claims are rejected.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to BRENDAN O. BAGGOT whose telephone number is (571)272-5265. The examiner can normally be reached on Monday through Thursday.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anne Marie Grunberg can be reached on 571/272-0975. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

/Anne Marie Grunberg/
Supervisory Patent Examiner, Art Unit 1638